

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 30, 2002, 12:33:38 ; Search time 21.5 Seconds
(without alignments)
4820.544 Million cell updates/sec

Title: US-10-025-514-8

Perfect score: 2675

Sequence: 1 MSGKSFAGVCPKPKSAQCL.....IEQNTKSPLEPMGVNPTOK 503

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phase.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rvirus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Length	ID	Description
1	2049.5	76.6	418	4 Q96ES1	Q96es1 homo sapien
2	2048.5	76.6	418	4 Q96BF9	Q96bf9 homo sapien
3	1908	71.3	396	6 O00394	O00394 cercopithe
4	1484.5	55.5	421	6 O46519	O46519 equus cabal
5	1480.5	55.3	413	11 O54761	O54761 spermophilu
6	1458.5	54.5	413	11 P97277	P97277 mesocricetu
7	1386	51.8	406	11 O64118	O64118 meriones un
8	1352	50.5	413	11 O8VC20	O8vc20 mus musculu
9	1346	50.3	410	11 Q91WH5	Q91wh5 mus musculu
10	1346	50.3	413	11 Q91XB8	Q91xb8 mus musculu
11	1346	50.3	413	11 Q91V74	Q91v74 mus musculu
12	1343.5	50.2	413	6 Q28665	Q28665 oryctolagus
13	1342	50.2	425	11 Q91XC1	Q91xc1 mus musculu
14	1335	49.9	413	11 O8VC41	O8vc41 mus musculu
15	1332	49.8	456	6 O62663	O62663 oryctolagus
16	1326.5	49.6	413	6 Q07298	Q07298 oryctolagus

17	1323	49.5	413	11	Q63969	Q63969 mus saxicol
18	1308.5	48.9	413	6	Q28666	Q28666 oryctolagus
19	1302.5	48.7	413	11	O54762	O54762 spermophilu
20	1196	44.7	413	11	O91X22	O91x22 mus musculu
21	1026	38.4	433	13	O9YIB8	O9yib8 xenopus lae
22	1010	37.8	197	4	Q13747	Q13747 homo sapien
23	850	31.8	420	11	Q60552	Q60552 mesocricetu
24	849	31.7	407	4	Q9UN09	Q9un09 homo sapien
25	845	31.6	410	13	Q90323	Q90323 cyprinus ca
26	829	31.0	418	11	O91X80	O91x80 mus musculu
27	828	31.0	418	11	O8VCH3	O8vch3 mus musculu
28	827	30.9	415	6	Q9GMA6	Q9gma6 sus scrofa
29	825	30.8	418	11	O91W80	O91w80 mus musculu
30	818	30.6	418	11	Q03734	Q03734 mus musculu
31	816	30.5	427	4	Q96B25	Q96b25 homo sapien
32	812	30.4	418	11	O62257	O62257 mus musculu
33	811.5	30.3	418	11	O91WP6	O91wp6 mus musculu
34	810.5	30.3	418	11	O62258	O62258 mus musculu
35	796	29.8	404	6	O9N212	O9n212 bos taurus
36	766.5	28.7	406	11	O88292	O88292 rattus norv
37	760	28.4	406	6	Q9GK37	Q9gk37 sus scrofa
38	758	28.3	411	11	O8R421	O8r421 rattus norv
39	757.5	28.3	416	6	Q27984	Q27984 bos taurus
40	745	27.9	418	11	O9D7D2	O9d7d2 mus musculu
41	742	27.7	412	11	O63556	O63556 rattus norv
42	726.5	27.2	413	11	O9CQ32	O9cq32 mus musculu
43	722.5	27.0	397	11	O91WQ0	O91wq0 mus musculu
44	714	26.7	423	11	P97569	P97569 rattus norv
45	673	25.2	371	6	Q9TTE1	Q9tte1 bos taurus

ALIGNMENTS

RESULT 1

Q96ES1 ID Q96ES1 PRELIMINARY; PRT; 418 AA.
AC Q96ES1
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE Similar to serine (or cysteine) proteinase inhibitor, clade A
DE (alpha-1 antiproteinase, antitrypsin), member 1.
DE Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=OVARY;
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -|- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
DR EMBL; BC011991; AAH11991.1; -.
DR InterPro; IPR000215; Serpin.
DR Pfam; PF00079; serpin; 1.
DR PROSITE; PS00284; SERPIN; UNKNOWN_1.
KW Serpin.
SQ SEQUENCE 418 AA; 46722 MW; 70165484573B7F16 CRC64;

Query Match 76.6%; Score 2049.5; DB 4; Length 418;
Best Local Similarity 97.5%; Pred. No. 3.5e-131;
Matches 398; Conservative 3; Mismatches 4; Indels 3; Gaps 1;

QY 96 GWCGRSCVSPVKAMDEPQGDAAQKTDTSHHDDHPTFNKIPNLAFAFSLYRLAHQSN 155
|:| |:| |
Db 14 GLC---CLVPVSLADEPQGDAAQKTDTSHHDDHPTFNKIPNLAFAFSLYRLAHQSN 70

QY 156 STNIFSPVSIATATAMLSLGTKADTHDEILEGNFNLTETPEAQIHGEGQELLRTNQ 215
|:| |:| |
Db 71 STNIFSPVSIATATAMLSLGTKADTHDEILEGNFNLTETPEAQIHGEGQELLRTNQ 130

QY 216 DSQQLTGTGNGLFSEGLKLVDFLEDKLYHSEAFVTFNGDTEAKKINDYVEKGTQ 275

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131 DSOQLTTGNGFLSEGLKLVDFLEDKYLYHSAFTVNFGEDEAKKQINDIVEKGTQ 190
190
276 GKIVDLVKELDRDTFALVNYIFFGKWERPEVKRDEEEDFHVQDQVTVTKVPMKRLGM 335
191 GKIVDLVKELDRDTFALVNYIFFGKWERPEVKRDEEEDFHVQDQVTVTKVPMKRLGM 250
336 FNIHQCKLSSWVLLMKYLGNAATFIFLPDEGKLOHLENELTHDITIKFLENERRSASL 395
251 FNIHQCKLSSWVLLMKYLGNAATFIFLPDEGKLOHLENELTHDITIKFLENERRSASL 310
396 HLPKLSITGTYDLKSVLGOLGKITKVFSGADLSGVTEAPLKLKSAVKAVLTIDEKGTG 455
311 HLPKLSITGTYDLKSVLGOLGKITKVFSGADLSGVTEAPLKLKSAVKAVLTIDEKGTG 370
456 AAGAMFLEAIPMSIPPEVKFNKPFVFLMTEQNTKSPFLMGKVVNPOTK 503
371 AAGAMFLEAIPMSIPPEVKFNKPFVFLMIDQNTKSPFLMGKVVNPOTK 418

RESULT 2
Q96BF9 PRELIMINARY; PRT; 418 AA.
AC Q96BF9;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DE Similar to serine (or cysteine) proteinase inhibitor, clade A (alpha-1
DE antiproteinase, antitrypsin), member 1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=COLON;
RA Strausberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
DR EMBL; BC015642; AALH5642.1; -.
DR InterPro; IPR000215; Serpin.
DR Pfam; PF00079; serpin; 1.
DR PROSITE; PS00284; SERPIN; UNKNOWN_1.
KW Serpin.
SQ SEQUENCE 418 AA; 46708 MW; FF0E525F303542AE CRC64;

Query Match 76.68; Score 2048.5; DB 4; Length 418;
Best Local Similarity 97.5%; Pred. No. 4.1e-131;
Matches 398; Conservative 2; Mismatches 5; Indels 3; Gaps 1;

QY 96 GWCGRKSCYSPVKAMEDPGDAAQKTDTSHDQDHTFNKIPNLAEFAFSLYRQLAHQSN 155
DB 14 GLC---CLVPSLAEDPGDAAQKTDTSHDQDHTFNKIPNLAEFAFSLYRQLAHQSN 70
QY 156 STNIFSPVSIATAFAMLSGLTKADTHDEILLEGFLNLTPEIPEAQIHEGFQELLRTLNQ 215
DB 71 STNIFSPVSIATAFAMLSGLTKADTHDEILLEGFLNLTPEIPEAQIHEGFQELLRTLNQ 130
QY 216 DSOQLTTGNGFLSEGLKLVDFLEDKYLYHSAFTVNFGEDEAKKQINDIVEKGTG 275
DB 131 DSOQLTTGNGFLSEGLKLVDFLEDKYLYHSAFTVNFGEDEAKKQINDIVEKGTG 190
QY 276 GKIVDLVKELDRDTFALVNYIFFGKWERPEVKRDEEEDFHVQDQVTVTKVPMKRLGM 335
DB 191 GKIVDLVKELDRDTFALVNYIFFGKWERPEVKRDEEEDFHVQDQVTVTKVPMKRLGM 250
QY 336 FNIHQCKLSSWVLLMKYLGNAATFIFLPDEGKLOHLENELTHDITIKFLENERRSASL 395
DB 251 FNIHQCKLSSWVLLMKYLGNAATFIFLPDEGKLOHLENELTHDITIKFLENERRSASL 310
QY 396 HLPKLSITGTYDLKSVLGOLGKITKVFSGADLSGVTEAPLKLKSAVKAVLTIDEKGTG 455
DB 311 HLPKLSITGTYDLKSVLGOLGKITKVFSGADLSGVTEAPLKLKSAVKAVLTIDEKGTG 370

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456 AAGAMFLEAIPMSIPPEVKFNKPFVFLMTEQNTKSPFLMGKVVNPOTK 503
371 AAGAMFLEAIPMSIPPEVKFNKPFVFLMTEQNTKSPFLMGKVVNPOTK 418

RESULT 3
O00394 PRELIMINARY; PRT; 396 AA.
AC O00394;
DT 01-JUL-1997 (Tremblrel. 04, Created)
DT 01-JUL-1997 (Tremblrel. 04, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE Alpha-1-antitrypsin (Fragment).
GN PI.
OS Cercopithecus aethiops (Green monkey) (Grivet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Cercopithecus.
OX NCBI_TaxID=9534;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=KIDNEY;
RA Yoshida K., Suzuki Y., Yamamoto K., Watanabe M., Sinohara H.;
RT "Cloning and sequencing of complementary DNAs encoding alpha-2-HS
RT glycoprotein, alpha-1-antitrypsin, and beta-actin from african green
RT monkey, Cercopithecus aethiops.";
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=KIDNEY;
RX MEDLINE=85026667; PubMed=6333329;
RA Colau B., Chuchana P., Bollen A.;
RT "Revised sequence of full-length complementary DNA coding for human
RT alpha 1-antitrypsin.";
RL DNA 3:327-330(1984).
CC -1- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
DR EMBL; AB004044; BAA20264.1; -.
DR HSSP; P01009; 9API.
DR InterPro; IPR000215; Serpin.
DR Pfam; PF00079; serpin; 1.
DR SMART; SM00093; SERPIN; 1.
DR PROSITE; PS00284; SERPIN; 1.
KW Serpin.
FT NON_TER
SQ SEQUENCE 396 AA; 44587 MW; 1042EABFAA0A2825 CRC64;

Query Match 71.3%; Score 1908; DB 6; Length 396;
Best Local Similarity 92.9%; Pred. No. 1.3e-121;
Matches 367; Conservative 19; Mismatches 9; Indels 0; Gaps 0;

QY 109 MEDPGDAAQKTDTSHDQDHTFNKIPNLAEFAFSLYRQLAHQSNSTNIFSPVSIAT 168
DB 2 VEDPGDAAQKTDTSHDQDHTFNKIPNLAEFAFSLYRQLAHQSNSTNIFSPVSIAT 61
QY 169 AFAMLSGLTKADTHDEILLEGFLNLTPEIPEAQIHEGFQELLRTLNQDLSQQLTTGNGLF 238
DB 62 AFAMLSGLTKADTHDEILLEGFLNLTPEIPEAQIHEGFQELLRTLNQDLSQQLTTGNGLF 121
QY 229 LSEGLKLVDFLEDKYLYHSAFTVNFGEDEAKKQINDIVEKGTGKIVDLVKELDRD 288
DB 122 LNKSVKVVDFLEDKYLYHSAFTVNFGEDEAKKQINDIVEKGTGKIVDLVKELDRD 181
QY 289 TVFALVNYIFFGKWERPEVKRDEEEDFHVQDQVTVTKVPMKRLGMFNTVHCKLSSWV 348
DB 182 TVFALVNYIFFGKWERPEVKRDEEEDFHVQDQVTVTKVPMKRLGMFNTVHCKLSSWV 241
QY 349 LLMKYLGNAATFIFLPDEGKLOHLENELTHDITIKFLENERRSASLHLPKLSITGTYDL 408
DB 242 LLMKYLGNAATFIFLPDEGKLOHLENELTHDITIKFLENERRSASLHLPKLSITGTYDL 301
QY 409 KSVLGOLGKITKVFSGADLSGVTEAPLKLKSAVKAVLTIDEKGTGAAGAMFLEAIPMS 468
DB 122 LNKSVKVVDFLEDKYLYHSAFTVNFGEDEAKKQINDIVEKGTGKIVDLVKELDRD 181

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KW Hypothetical protein; Protease.
SQ SEQUENCE 413 AA; 45896 MW; 12C19B63AAD5E66E CRC64;

Query Match      50.5%; Score 1352; DB 11; Length 413;
Best Local Similarity 62.6%; Pred. No. 7.8e-84;
Matches 256; Conservative 73; Mismatches 70; Indels 10; Gaps 4;

QY 96 GCMGKSCVSPVKAMEDPOGDAAQKTDTSHHDDHPTFNKIPNLAEAFSLYROLAHQSN 155
DB 14 GLC---CLVPSFLAED-----VQETDTSQKQDS-PASHEIATNLGDFALISLYRELHVQSN 64

QY 156 STNIFSPSVIATAFAMLSLGTAKDTHDEILGLNFIETPEAQIHGFGFELLRTLNQ 215
DB 65 TSNIFFSPSVIATAFAMLSLGSKGDTHTQILEGLQFNLTQTSADIIHKSFOHLLQTLNRP 124

QY 216 DSQQLTTGNGFLSEGLKLVKDFLEDDYKLYHSEAFVNFQDTEBEAKKQINDYVEKGTQ 275
DB 125 DSELQSTGNGFLVNDLKLVEKAEKNHYQAEVSVNFAESEAAYKINDVEKGTQ 184

QY 276 GKIVDLVKELDRDTVFALVNYIFFGKWKERPFEVKDTEEDDFHVDQVTVKVPMMKRLGM 335
DB 182 GRIVEAVKELDDQTVFALANVILFKGKWKPFDPENTEEAEFFHVDSTTVKVPMMKRLGM 241

QY 336 FNIQCKKLSWVLLMKYLGNAITAFILPDGKQLQHLNELTHDIIITKFLNEDRRSASL 395
DB 242 LDVHHCSTLSSWVLLMDYAGNATAVFLPDGKMQHLEQTLSEKLSKFLNRRRLAQI 301

QY 396 HLPKLSITGTYDLKSVLQGLGTTKVFSGADLSGVTEE-APLKLSKAVHKAVALTIDEKGT 454
DB 302 HPRLSISGTYDLKSVLQGLGTTKVFSGADLSGVTEE-APLKLSKAVHKAVALTIDEKGT 361

QY 455 EAAGAMFLEATPMSIPPEVKFNKPFVFLMIEQNTKSPFLMGKVVNPTQK 503
DB 362 EAAAVTVLLAVPYSMPILRFDPHFLFIIEEHTQSPFLMGKVVNPTQK 410

RESULT 10
QY1XB8
ID QY1XB8 PRELIMINARY; PRT; 413 AA.
AC QY1XB8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Similar to serine protease inhibitor 1-1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
DR EMBL; BC011040; AAH11040.1; -.
DR InterPro; IPR000215; Serpin.
DR Pfam; PF00079; serpin_1
DR PROSITE; PS00284; SERPIN; UNKNOWN_1.
KW Protease; Serpin.
KW NON_TER
SQ SEQUENCE 413 AA; 45966 MW; ALFDA1B0C96DFDCC CRC64;

Query Match      50.3%; Score 1346; DB 11; Length 413;
Best Local Similarity 62.3%; Pred. No. 2e-83;
Matches 255; Conservative 72; Mismatches 72; Indels 10; Gaps 4;

QY 96 GCMGKSCVSPVKAMEDPOGDAAQKTDTSHHDDHPTFNKIPNLAEAFSLYROLAHQSN 155
DB 14 GLC---CLVPSFLAED-----VQETDTSQKQDS-PASHEIATNLGDFALISLYRELHVQSN 64

QY 156 STNIFSPSVIATAFAMLSLGTAKDTHDEILGLNFIETPEAQIHGFGFELLRTLNQ 215
DB 65 TSNIFFSPSVIATAFAMLSLGSKGDTHTQILEGLQFNLTQTSADIIHKSFOHLLQTLNRP 124

QY 216 DSQQLTTGNGFLSEGLKLVKDFLEDDYKLYHSEAFVNFQDTEBEAKKQINDYVEKGTQ 275
DB 125 DSELQSTGNGFLVNDLKLVEKAEKNHYQAEVSVNFAESEAAYKINDVEKGTQ 184

QY 276 GKIVDLVKELDRDTVFALVNYIFFGKWKERPFEVKDTEEDDFHVDQVTVKVPMMKRLGM 335
DB 185 GKTAEAVKELDDQTVFALANVILFKGKWKPFDPENTEEAEFFHVDSTTVKVPMMKRLGM 244

QY 336 FNIQCKKLSWVLLMKYLGNAITAFILPDGKQLQHLNELTHDIIITKFLNEDRRSASL 395
DB 245 LDVHHCSTLSSWVLLMDYAGNATAVFLPDGKMQHLEQTLSEKLSKFLNRRRLAQI 304

QY 396 HLPKLSITGTYDLKSVLQGLGTTKVFSGADLSGVTEE-APLKLSKAVHKAVALTIDEKGT 454
DB 302 HPRLSISGTYDLKSVLQGLGTTKVFSGADLSGVTEE-APLKLSKAVHKAVALTIDEKGT 361

RESULT 9
QY1WH5
ID QY1WH5 PRELIMINARY; PRT; 410 AA.
AC QY1WH5;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical 45.6 kDa protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RA Strausberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
DR EMBL; BC015266; AAH15266.1; -.
DR InterPro; IPR000215; Serpin.
DR Pfam; PF00079; serpin_1
DR PROSITE; PS00284; SERPIN; UNKNOWN_1.
KW Hypothetical protein; Serpin.
KW NON_TER
SQ SEQUENCE 410 AA; 45622 MW; ED142591DB58F5E2 CRC64;

Query Match      50.3%; Score 1346; DB 11; Length 410;
Best Local Similarity 62.8%; Pred. No. 2e-83;
Matches 257; Conservative 70; Mismatches 72; Indels 10; Gaps 4;

QY 96 GCMGKSCVSPVKAMEDPOGDAAQKTDTSHHDDHPTFNKIPNLAEAFSLYROLAHQSN 155
DB 11 GLC---CLVPSFLAED-----VQETDTSQKQDS-PASHEIATNLGDFALISLYRELHVQSN 61

QY 156 STNIFSPSVIATAFAMLSLGTAKDTHDEILGLNFIETPEAQIHGFGFELLRTLNQ 215
DB 62 TSNIFFSPSVIATAFAMLSLGSKGDTHTQILEGLQFNLTQTSADIIHKSFOHLLQTLNRP 121
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Db 305 HPPRLSISGEYNLTKLMSPLGTRIFNNGADLSGITEENAPLKLQAVHKAVLTIDETGT 364
QY 455 EAAGAMELEAIPMSIPPEVKFNKPFVFLMIEQNTKSPFLFMGVNPTQK 503
Db 365 EAAAVTVLQWPMSPMPILRDHPFLFIIFEHTQSPFLFVGKVDPTHK 413
RESULT 12
Q28665 PRELIMINARY; PRT; 413 AA.
ID Q28665
AC Q28665;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Unknown (Protein for MGC:13995) (Similar to serine protease inhibitor
1-3) (Protein for MGC:13994) (Hypothetical 46.0 kDa protein).
DE 1-3 (Protein for MGC:13994) (Hypothetical 46.0 kDa protein).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RA Strausberg R.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RA Strausberg R.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
DR EMBL; BC011041; AAH11041.1; -
DR EMBL; BC009818; AAH09818.1; -
DR EMBL; BC010984; AAH10984.1; -
DR EMBL; BC021780; AAH21780.1; -
DR EMBL; BC021325; AAH21325.1; -
DR EMBL; BC024108; AAH24108.1; -
DR InterPro; IPR000215; Serpin.
DR Pfam; PF00079; serpin; 1.
DR PROSITE; PS00284; SERPIN; 1.
KW Hypothetical protein; Protease; Serpin.
FT SIGNAL 1 23 POTENTIAL.
FT CHAIN 24 413 ALPHA-1-ANTITRYPSIN E.
SQ SEQUENCE 413 AA; 45684 MW; COE86D60916639E2 CRC64;
Query Match 50.2%; Score 1343.5; DB 6; Length 413;
Best Local Similarity 63.3%; Pred. No. 2e-83;
Matches 257; Conservative 61; Mismatches 83; Indels 5; Gaps 1;
QY 97 MCGKSCVSPVKAMEDPQGDAAQKTDTHSHDQDHTFNKIPNLAEFAFSLYRQLAHQSN 156
Db 12 LAGLGLLP-----GFLADEAQETAVSHEQDHPACHRIAPSLAEFALSLYREVAHESNT 66
QY 157 TNIFSPVSIATAFAMLSLGTADTHDEILGLNFNLTPEAQIHGFEQLLRLNPD 216
Db 67 TNIFSPVSIATAFAMLSLGTADTHDEILGLNFNLTPEAQIHGFEQLLRLNPD 126
QY 217 SLOLTTGNGLFSEGLKLVDFLEVDKLYHSEAFVNFNGDTEEAQKQINDYVEKGTQ 276
Db 127 SELQALGALVFNHVKLQKHLFLEDAKLYSEAFVNFNGDTEEAQKQINDYVEKGTQ 186
QY 277 KIVDLVKELDRDTVFALVNYIFFKQKWERPFVFKDTEEDFHVQDVTYVPMKRLGMF 336
Db 187 KIVDLVKELDRDTVFALVNYIFFKQKWERPFVFKDTEEDFHVQDVTYVPMKRLGMF 246
QY 337 NIOHCKLSSWLLMKYLGNAITAFPLDSEGLKLVDFLEVDKLYHSEAFVNFNGDTEEAQKQINDYVEKGTQ 396
Db 247 VMFHCSTLSTVLMYDKNATLFLDPEGLKLVDFLEVDKLYHSEAFVNFNGDTEEAQKQINDYVEKGTQ 306
QY 397 LPKLSITGTVDLKSGLGQITGVFNSGADLSGITEENAPLKLQAVHKAVLTIDETGT 456
Db 307 FPKLSISGYDLKPLGLKGLITGVFNSGADLSGITEENAPLKLQAVHKAVLTIDETGT 366
QY 457 AGAMFLEAIPMSIPPEVKFNKPFVFLMIEQNTKSPFLFMGVNPTQK 502
Db 367 EAAAVTVLQWPMSPMPILRDHPFLFIIFEHTQSPFLFVGKVDPTHK 412
RESULT 13
Q91XCI

Db 305 HPPRLSISGEYNLTKLMSPLGTRIFNNGADLSGITEENAPLKLQAVHKAVLTIDETGT 364
QY 455 EAAGAMELEAIPMSIPPEVKFNKPFVFLMIEQNTKSPFLFMGVNPTQK 503
Db 365 EAAAVTVLQWPMSPMPILRDHPFLFIIFEHTQSPFLFVGKVDPTHK 413
RESULT 11
Q91V74 PRELIMINARY; PRT; 413 AA.
ID Q91V74
AC Q91V74;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Unknown (Protein for MGC:13995) (Similar to serine protease inhibitor
1-3) (Protein for MGC:13994) (Hypothetical 46.0 kDa protein).
DE 1-3 (Protein for MGC:13994) (Hypothetical 46.0 kDa protein).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RA Strausberg R.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RA Strausberg R.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
DR EMBL; BC011041; AAH11041.1; -
DR EMBL; BC009818; AAH09818.1; -
DR EMBL; BC010984; AAH10984.1; -
DR EMBL; BC021780; AAH21780.1; -
DR EMBL; BC021325; AAH21325.1; -
DR EMBL; BC024108; AAH24108.1; -
DR InterPro; IPR000215; Serpin.
DR Pfam; PF00079; serpin; 1.
DR PROSITE; PS00284; SERPIN; UNKNOWN.1.
KW Hypothetical protein; Protease; Serpin.
FT SIGNAL 1 23 POTENTIAL.
FT CHAIN 24 413 ALPHA-1-ANTITRYPSIN E.
SQ SEQUENCE 413 AA; 45951 MW; 858FA3BF10ABC1B8 CRC64;
Query Match 50.3%; Score 1346; DB 11; Length 413;
Best Local Similarity 62.8%; Pred. No. 2e-83;
Matches 257; Conservative 70; Mismatches 72; Indels 10; Gaps 4;
QY 96 MCGKSCVSPVKAMEDPQGDAAQKTDTHSHDQDHTFNKIPNLAEFAFSLYRQLAHQSN 155
Db 14 GLC---CLVPFLAE-----VQETDTSQKQDS-PASHEIATNLGDFALSILYRELHVSQ 64
QY 156 STNIFSPVSIATAFAMLSLGTADTHDEILGLNFNLTPEAQIHGFEQLLRLNPD 215
Db 65 TSNIFFSPVSIATAFAMLSLGTADTHDEILGLNFNLTPEAQIHGFEQLLRLNPD 124
QY 216 DSLOLTTGNGLFSEGLKLVDFLEVDKLYHSEAFVNFNGDTEEAQKQINDYVEKGTQ 275
Db 125 DSELQALGALVFNHVKLQKHLFLEDAKLYSEAFVNFNGDTEEAQKQINDYVEKGTQ 184
QY 276 KIVDLVKELDRDTVFALVNYIFFKQKWERPFVFKDTEEDFHVQDVTYVPMKRLGMF 335
Db 185 KIVDLVKELDRDTVFALVNYIFFKQKWERPFVFKDTEEDFHVQDVTYVPMKRLGMF 244
QY 336 FNIQCHCKLSSWLLMKYLGNAITAFPLDSEGLKLVDFLEVDKLYHSEAFVNFNGDTEEAQKQINDYVEKGTQ 395
Db 245 LDVHCHCKLSSWLLMKYLGNAITAFPLDSEGLKLVDFLEVDKLYHSEAFVNFNGDTEEAQKQINDYVEKGTQ 304
QY 396 HPPRLSISGEYNLTKLMSPLGTRIFNNGADLSGITEENAPLKLQAVHKAVLTIDETGT 454
Db 307 FPKLSISGYDLKPLGLKGLITGVFNSGADLSGITEENAPLKLQAVHKAVLTIDETGT 366


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ID Q91XC1 PRELIMINARY; PRT; 425 AA.
AC Q91XC1;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Unknown (Protein for IMAGE:4210562) (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
DR EMBL; BC010988; AAH10988.1; -.
DR InterPro; IPR000215; Serpin.
DR Pfam; PF00079; serpin; 1.
DR SMART; SM00284; SERPIN; 1.
DR PROSITE; PS00284; SERPIN; UNKNOWN_1.
KW Serpin.
ET NON_TER
SQ SEQUENCE 425 AA; 47157 MW; EA9E50E40C33CAFC CRC64;

Query Match 50.2%; Score 1342; DB 11; Length 425;
Best Local Similarity 62.6%; Pred. No. 3.9e-83;
Matches 256; Conservative 70; Mismatches 73; Indels 10; Gaps 4;

QY 96 GCGKSCVSPVKAMEDPQGDAAKTDTSHTDQDHTFNKIPNLAFAFSLYRLAQHSN 155
DB 26 GLC---CLVPNLAED-----VQETDTSQKQDS-PASHEIATNLGDFALISLYRELVLHQS 76
QY 156 STNIFSPVSIATAFAMLSGLTKADTHDEILGLNPNLTETPEAQIHGFGQELLRTNQ 215
DB 77 TSNIFSPVSIATAFAMLSGLSKGDTHTQILEGLQFNLTQTAEDIHKSFOHLLQTLNRP 136
QY 216 DSQQLTGTGNGLSGLKLVKDYKLFEDYKLYHSEAFVNFQDTEEAKKOINDYVEKGTQ 275
DB 137 DSELQSLTGNGLVNNDLKLVEKLEAKNHYQAEVSVNFAESEAKKVINDFVEKGTQ 196
QY 276 GKIVDLVKELDRDTVFALVNYIFFKQKWERPFVKDTEEDFHVQDVTTKVPMKRLGM 335
DB 197 GIAEAVKLDQDTVFALANTILFKGKWKPPDPENTEAEAEHFVDESTTVKVPMTLSGM 256
QY 336 FNIQCHCKLSSVLLMKYLGNTAIFFLPDGKQHLQENELTHDITTKFLENEDRRSASL 395
DB 257 LDVHHCSTLSSVLLMDYAGNATAVFLPDGKQHLQENELTHDITTKFLENEDRRSASL 316
QY 396 HLPKLSITGYDLKSVLGQGITKVFSGADLSGVTER-APLKLSKAVHKAVLTIDEKGT 454
DB 317 HPRLSISGEYNLKTLSPLGITRIFNNGADLSGITEENAPLKLSQAVHKAVLTIDEKGT 376
QY 455 EAAGAMFLEAIPMSIPPEVFNKPFVFLMIQNTKSPFLMGKVVNPTOK 503
DB 377 EAAAVTVLLAVPYSMPILRDHPFLFIIFEHTQSPFLFGKVVDPDTHK 425

RESULT 14
Q8VC41 PRELIMINARY; PRT; 413 AA.
AC Q8VC41;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Similar to serine protease inhibitor 1-4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RA Strausberg R.;
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RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC021850; AAH21850.1; -.
DR InterPro; IPR000215; Serpin.
DR Pfam; PF00079; serpin; 1.
DR SMART; SM00093; SERPIN; 1.
DR PROSITE; PS00284; SERPIN; UNKNOWN_1.
KW Protease.
SQ SEQUENCE 413 AA; 45995 MW; C96A4EC0A7951872 CRC64;

Query Match 49.9%; Score 1335; DB 11; Length 413;
Best Local Similarity 62.3%; Pred. No. 1.1e-82;
Matches 255; Conservative 69; Mismatches 75; Indels 10; Gaps 4;

QY 96 GCGKSCVSPVKAMEDPQGDAAKTDTSHTDQDHTFNKIPNLAFAFSLYRLAQHSN 155
DB 14 GLC---CLVPNLAED-----VQETDTSQKQDS-PASHEIATNLGDFALISLYRELVLHQS 64
QY 156 STNIFSPVSIATAFAMLSGLTKADTHDEILGLNPNLTETPEAQIHGFGQELLRTNQ 215
DB 65 TSNIFSPVSIATAFAMLSGLSKGDTHTQILEGLQFNLTQTAEDIHKSFOHLLQTLNRP 124
QY 216 DSQQLTGTGNGLSGLKLVKDYKLFEDYKLYHSEAFVNFQDTEEAKKOINDYVEKGTQ 275
DB 125 DSELQSLTGNGLVNNDLKLVEKLEAKNHYQAEVSVNFAESEAKKVINDFVEKGTQ 184
QY 276 GKIVDLVKELDRDTVFALVNYIFFKQKWERPFVKDTEEDFHVQDVTTKVPMKRLGM 335
DB 185 GKIVAEVKELDQDTVFALANYILFKGKWKPPDPENTEAEAEHFVDESTTVKVPMTLSGM 244
QY 336 FNIQCHCKLSSVLLMKYLGNTAIFFLPDGKQHLQENELTHDITTKFLENEDRRSASL 395
DB 245 LDVHHCSTLSSVLLMDYAGNATAVFLPDGKQHLQENELTHDITTKFLENEDRRSASL 304
QY 396 HLPKLSITGYDLKSVLGQGITKVFSGADLSGVTER-APLKLSKAVHKAVLTIDEKGT 454
DB 305 HPRLSISGEYNLKTLSPLGITRIFNNGADLSGITEENAPLKLSKAVHKAVLTIDEKGT 364
QY 455 EAAGAMFLEAIPMSIPPEVFNKPFVFLMIQNTKSPFLMGKVVNPTOK 503
DB 365 EAAAVTVLLAVPYSMPILRDHPFLFIIFEHTQSPFLFGKVVDPDTHK 413

RESULT 15
O62663 PRELIMINARY; PRT; 456 AA.
AC O62663;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE AFS-22.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RA Saito A.;
RT "Protease inhibitory activity of recombinant alpha-1-antitrypsinases expressed in Escherichia coli.";
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
DR EMBL; AB015164; BAA28760.1; -.
DR HSSP; P01009; 8AP1.
DR InterPro; IPR000215; Serpin.
DR Pfam; PF00079; serpin; 1.
DR SMART; SM00093; SERPIN; 1.
DR PROSITE; PS00284; SERPIN; UNKNOWN_1.
KW Serpin.
SQ SEQUENCE 456 AA; 50542 MW; 88E19DF2767F5C07 CRC64;

Query Match 49.8%; Score 1332; DB 6; Length 456;
Best Local Similarity 58.8%; Pred. No. 2e-82;
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Conservative	65	Mismatches	105	Indels	16	Gaps	4
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[illegible]

Search completed: November 30, 2002, 12:36:43
Job time : 23.5 secs